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# Genetic parameters estimation and evaluation of yield and yield attributing traits of rice genotypes under reproductive drought stress condition

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In order to determine the degree of genetic divergence and to assess yield and yield components of rice under reproductive drought stress conditions, a field screening of eleven genotypes was carried out at a farmer's field in Sundarbazar, Lamjung. This was done using a randomized complete block design with three replications. Significant variations between all genotypes for all tested parameters were found by the analysis of variance, indicating the presence of genetic variability as well as the possibility of future improvement through selection. Phenotypic coefficient of variance was higher than genotypic coefficient of variance for all traits under study and difference between them was found low, meaning less influence of environment in the expression of these characters and selection could be effective on the basis of phenotype independent of genotype for the improvement of these traits. Moderate to high estimates of GCV, PCV, heritability and genetic advance as percent of mean was found for all traits studied. Chlorophyll content, leaf area and filled grains per panicle showed positive and significant association with grain yield. Three principal components were extracted based on eigen value accounting 84% of

**total variation. Eleven rice genotypes were clustered into three groups where cluster 3 was found to be superior for yield and yield attributing traits. Eight genotypes yielded more than that of check variety where highest yield was recorded by Sukhadhan-4. Rice genotypes under study showed enough genetic diversity hence, indirect selection of traits like flag leaf area, filled grains per panicle, harvest index, plant height, SPAD value and thousand grain weights will be effective for increasing yield.**

**Key words:** rice, reproductive, stress, drought, correlation, heritability, cluster

## INTRODUCTION

Rice (*Oryza sativa* L.) is a self –pollinated cereal crop which is the staple cereal crop, feeding more than 3.5 billion global population (IRRI, 2017). It belongs to Graminae family having chromosome number  $2n=24$ . It is majorly grown in tropical and sub-tropical climate. It is cultivated in 114 countries and it is the source of income for more than 100million household in Asia (Kumar et al., 2015). Rice is the 3<sup>rd</sup> largest produced agricultural commodity globally, after wheat and maize in terms of their production (NGS, 2017). Globally, rice production and consumption moves in tandem. Its annual production was 741.4 million ton worldwide (FAOSTAT, 2017). Asia has high dependency on rice as it produces and consumes more than 90% of rice. It is the major stable cereal crop for majority of people living in this continent including 560 million poor (GRiSP, 2013). China and India are the leading producers and consumers of paddy rice worldwide. India is the largest exporter of rice followed by Thailand and Vietnam (The statistics portal, 2018).

Nepal is considered to be one of the important center for rice genetic resources. According to Mallick, 1981, more than 1,700 rice landraces are reported. Rice in Nepal can grow from 60 to 3,050 m altitude. It is believed that commercial production started about 500 years ago in Nepal. More than 3,980 germplasm has been conserved by Nepal Agriculture Research Council (NARC) which were collected from national and international sources (MOAD,2015). Rice accounts 42.5% of the total area and 51.6% on total production of food grains (MOAD,2013). Rice contributes highest in terms of area, production and productivity among cereal crops which were 13, 62,908ha, 42, 99,087 metric tons and 3.15 MT/ha respectively .It provides 40% of the food calorie to the Nepalese people and contributes almost 20% to the agricultural gross domestic product (AGDP) and nearly 7% to GDP. Drought stress coinciding with reproductive stage reduces the yield drastically.

Globally, 18 million tons of rice production is decreased annually due to drought condition (Haider et al., 2012). For increasing productivity, reducing risk and alleviating poverty in communities, there is need for the development of rice varieties with improved drought tolerance which are dependent on rain fed production.

## MATERIALS AND METHODS

### Design of the research and experimental layout

In a farmer's field in Sundarbazar, Lamjung, an experimental trial involving 11 genotypes—namely, Mansuli, Ghaiya, Radha-12, Sukhadhan-4, Loktantra, Sukhadhan-3, Chaite-2, Sabitri (Local Check), Radha-9, NR-1488, and Sukhadhan-6—was carried out using a randomized complete block design (RCBD) with three replications. Thus, there were 33 total plots, each measuring  $1.2 \times 2$  m<sup>2</sup>, with a 50 cm distance between them.

### **Nursery preparation and management**

Nursery bed was prepared at campus quarter premises. Fine soil was prepared by the help of by broadcasting. RARS, Khajura provided the source seed for the research.

### **Preparation of rice field**

The experimental plot was ploughed two times with the help of tractor followed by levelling and puddling along with removal of weeds. After that, layout of field was done by making 33 plots manually using tapes, spades and pegs.

### **Nutrient management**

FYM was used at the rate of 6 ton/ha. Chemical fertilizers were supplied by applying urea, DAP, and MOP at the rate of 60:40:30 kilogram/hectare as recommended by NARC. DAP and MOP was used completely during the basal dose whereas urea was given in split dose i.e. half in basal dose and  $\frac{1}{4}$  of urea at 25 DAT and remaining  $\frac{1}{4}$  at 45 DAT.

### **Transplanting**

25 days old seedlings were transplanted at 20×20 cm in main field. Each hill consists of 2-3 seedlings.

### **Weed management**

Manual hand weeding was done on 25 and 45 DAT and after each weeding, top dressing of urea was done.

### **WATER MANAGEMENT**

Vegetative stage of rice was provided with sufficient water. Drought condition was created after 30 DAT until harvesting to induce stress at reproductive stage.

### **Harvesting of rice**

With the help of a sickle, harvesting from net plots was done manually. Following harvest, plants were kept on the field for 4 days to allow for sun drying. Then threshing and winnowing was performed. At 12% moisture content, the weight of the grains was recorded.

### **Data observation and recording**

Collection of data was done from five randomly chosen plants from each plot. Border plants were neglected. Flag leaf area (60 DAT), chlorophyll content (60 DAT), plant height (90 DAT), panicle length, thousand grain weight, harvest index, Days to booting (50%), Days to heading (50%), Days to flowering (50%), filled grain per panicle, fertility percentage, effective tiller per square meter, maturity days, and grain yield (ton/ha) were measured.

## RESULTS AND DISCUSSION

Significant differences for all traits studied were observed as revealed by analysis of variance (ANOVA), which suggests prevalence of ample genetic variability (Table 1 and table 2). Thus, selection is effective for the improvement of genotypes under study. The study revealed that Sukhadan-4 has highest mean yield with 40.44% more yield than local check (Sabitri), also it is best in terms of flag leaf area, filled grains per panicle, chlorophyll content, thousand grain weight, panicle length, fertility percent and effective tillers per meter square.

**Table 1. ANOVA for Yield and Yield components of rice**

Genotype	FGPP	HI	TW	PL	F%	ETM	GY
01.Mansuli	181.67bcd	0.23 d	17.18 e	23.60 bc	89.25 ab	75.31 abc	3.33de
02.Ghaiya	115.06e	0.34 bc	22.07 bcd	24.63 ab	77.01 cd	66.85 cd	3.03e
03.Radha-12	177.20cde	0.29 c	22.08 bcd	25.32 ab	83.24 abc	72.26 abc	4.42abc
04.Sukhadhan-4	260.63a	0.38 b	26.60 a	26.36 ab	88.77 ab	77.05 ab	5.00a
05.Loktantra	214.73abc	0.34 bc	20.45 cde	27.17 a	87.20 abc	75.69 abc	4.18abcd
06.Sukhadhan-3	174.33cde	0.46 a	23.86 abc	24.27 ab	91.92 a	79.79 a	3.85bcde
07.Chaite-2	168.80cde	0.39 b	25.05 ab	24.23 ab	88.53 abc	76.84 ab	3.97bcde
08.Sabitri	120.40de	0.28 cd	20.60 cde	20.98 c	69.10 d	59.98 d	3.56cde
09.Radha-9	136.06de	0.39 b	24.79 ab	25.86 ab	78.35 bcd	68.01 bcd	4.42abc
10.NR-1488	255.53ab	0.30 c	19.77 de	26.30 ab	89.97 a	80.60 a	4.43abc
11.Sukhadhan-6	258.45a	0.40 ab	24.71 ab	24.32 ab	87.26 abc	70.17 bc	4.50ab
F test	***	***	***	*	**	**	**
L.S.D (5%)	66.05	0.059	3.38	2.81	10.93	8.26	0.84
CV%	20.68	9.98	8.85	6.66	7.59	6.65	12.15
<b>Grand Mean</b>	<b>187.53</b>	<b>0.351</b>	<b>22.47</b>	<b>24.82</b>	<b>84.6</b>	<b>72.96</b>	<b>4.06</b>

\*\*\* Significant at  $p < 0.001$ , \*\* Significant at  $p < 0.01$ , \* Significant at  $p < 0.05$

FGPP=filled grain per panicle, HI= harvest index, TW= thousand grain weight, PL= panicle length, F%=fertility percent, ETM= effective tiller per meter, GY= grain yield

**Table 2. ANOVA for agro-morphological traits of rice**

Genotype	PH	FD	HD	BD	LA	SPAD	MD
01.Mansuli	129.16 b	112.67 a	111.67 a	102.33 b	49.77ab	32.55 cd	149.67 a
02.Ghaiya	115.46 c	83.67 e	82.00 e	74.33 f	37.67c	30.32 d	134.00 c
03.Radha-12	115.74 c	115.33 a	114.00 a	106.33 ab	54.33ab	38.71 a	152.67 a
04.Sukhadhan-4	111.41 cd	89.67 d	85.34 d	80.67 e	57.23a	37.02 ab	139.67 b
05.Loktantra	138.80 b	102.34 c	100.67 c	90.33 d	47.10b	35.00 bc	134.67 c
06.Sukhadhan-3	113.60 c	90.00 d	86.00 d	81.00 e	35.56c	38.60 a	131.33 cd
07.Chaite-2	99.99 de	89.00 d	88.00 d	81.00 e	37.12c	38.64 a	128.33 d
08.Sabitri	98.70 e	116.00 a	113.67 a	109.67 a	35.41c	37.38 ab	154.00 a
09.Radha-9	103.90cde	102.34 c	100.34 c	91.00 d	50.87ab	38.70 a	151.33 a
10.NR-1488	164.92 a	108.67 b	107.33 b	97.33 c	55.67ab	38.80 a	153.67 a
11.Sukhadhan-6	103.63 cde	88.67 d	86.67 d	80.33 e	56.66ab	38.56 a	134.00 c
F test	***	***	***	***	***	***	***
L.S.D (5%)	11.42	3.17	2.82	4.19	8.47	2.47	4.4
CV%	5.69	1.86	1.69	2.72	10.58	3.94	1.82
<b>Grand Mean</b>	<b>117.75</b>	<b>99.84</b>	<b>97.78</b>	<b>90.39</b>	<b>47.03</b>	<b>36.75</b>	<b>142.12</b>

\*\*\* Significant at  $p < 0.001$

PH=plant height 90DAT, FD= Days to 50% flowering, HD= Days to 50% heading, BD=Days to 50% booting after sowing, LA=Flag leaf area 60 DAT, SPAD = chlorophyll content 60DAT, MD=maturity days

**Table 3. Correlation analysis between grain yield and other traits**

Traits	LA	SPAD	FGPP	GY	PH	PL	TW	HI	BD	HD	FD	F%	ETM	MD
LA	1													
SPAD	.234	1												
FGPP	.735*	.325	1											
GY	.729*	.688*	.715*	1										
PH	.360	-.148	.452	.068	1									
PL	.574	.066	.530	.591	.517	1								
TW	.063	.464	.150	.551	-.599	.214	1							
HI	-.131	.422	.149	.376	-.399	.270	.843**	1						
BD	.132	.160	-.163	-.060	.210	-.325	-.639*	-.758**	1					
HD	.187	.111	-.139	-.063	.319	-.211	-.699*	-.785**	.985**	1				
FD	.192	.135	-.125	-.033	.306	-.214	-.675*	-.763**	.990**	.997**	1			
F%	.355	.186	.708*	.367	.431	.515	.087	.296	-.336	-.281	-.281	1		
ETM	.278	.205	.626*	.360	.560	.589	.041	.243	-.264	-.203	-.199	.948**	1	
MD	.361	.142	-.112	.085	.267	-.143	-.480	-.688*	.853**	.855**	.866**	-.397	-.295	1

\*Correlation is significant at the 0.05 level (2-tailed). \*\*Correlation is significant at the 0.01 level (2-tailed).

LA= flag leaf area 60 DAT, SPAD=chlorophyll content 60DAT, PH=plant height 90DAT, PL=panicle length, TW=thousand grain weight, HI= harvest index, BD=Days to 50% booting, HD= Days to 50% heading, FD= Days to 50% flowering, FGPP=filled grain per panicle, F%=fertility percent, ETM=effective tiller per meter square, MD=maturity days, GY=grain yield

### Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV)

High GCV and PCV was observed for FGPP followed by LA, HI, PH, BD, MD, TW and FD (Table 3). Similarly relatively moderate values of GCV and PCV was observed for ETM followed by F%, SPAD, MD and PL. Above results were in consistent with findings of [Abebe et al. \(2017\)](#) for PH; [Abarshahr et al. \(2011\)](#) and [Abebe et al. \(2017\)](#) for TW; [Mukherjee et al. \(2018\)](#) for FD and FGPP. Similarly for moderate GCP and PCV, similar results were found by [Abarshahr et al. \(2011\)](#) for PL; [Padmaja et al. \(2008\)](#) for F% and [Mukherjee et al. \(2018\)](#) for ETM. The coefficient of variation revealed that for most of the traits high GCV was recorded which signifies present of high variation among genotypes with respect to these characters and also PCV was higher than GCV for all traits under study and difference between them was found low, meaning less impact of environment in the expression of these characters and selection could be effective on the basis of phenotype for the improvement of these traits.

### Heritability (broad sense)

Heritability estimates provides the reliable information of genetic variability out of total variability that is transmissible to next generation. Hence, it is used in expressing the reliability of phenotypic value. Therefore, the high heritability is suitable for selection of traits. It was found that heritability estimates ranged from 99% for BD, HD, FD to 74% for PL. High heritability was observed for all the traits studied. Highest heritability was found HD, BD, FD followed by MD, PH, SPAD, HI, LA, TW, FGPP, ETM, GY, F% and PL. Above results were in consistent with the findings of [Rahman et al. \(2012\)](#) for LA, HI, GY and FD.

Similarly results were found by [Abarshahr et al. \(2011\)](#) for GY, PH, PL, FD, LA and F%; [Mukherjee et al. \(2018\)](#) for FGPP ; [Ukaoma et al.\(2013\)](#) for ETM and [Longjam & Singh\(2019\)](#) for TW.

#### Genetic advance (GA) and genetic advance as percentage of mean (GAM)

Information about the necessary improvement in the genotypic value of the new population over the old population is provided by genetic advance. However, estimates of genetic advance as percentage of the mean offer more trustworthy information about the role of selection in enhancing traits. Genetic advance expressed as percentage of mean (GAM) ranged from 19.72% for PL to 91.06% for FGPP. High genetic advance as percentage of mean was observed for all the traits studied except PL. Highest value of GAM was observed for FGPP followed by HI, LA, PH, BD, HD, GY, FD, TW, SPAD, ETM, MD , F% and PL. Moderate GAM was recorded for PL. Above results were in consistent with the findings of Bornrare et al.(2014) for ETM, GY and PH; [Mukherjee et al.\(2018\)](#) for FD and F%; [Abarshahr et al. \(2011\)](#) for GY, FGPP and PH; [Rahman et al.\(2012\)](#) for LA and HI; [Ukaoma et al.\(2013\)](#) for ETM; [Padmaja et al.\(2018\)](#) for TW and [Abebe et al. \(2017\)](#) for PL.

Heritability estimates alone is not appropriate; instead, choosing superior varieties, which is the contribution of additive gene action, requires high heritability combined with high GAM. High heritability along with high genetic advance expressed as percentage of mean was found for traits such as HI, LA, PH, FGPP, BD and HD, which indicates that heritability is due to the additive gene action and selection may be effective for such traits. While low heritability along with low GAM was found in traits like F% and PL indicating non-additive gene action and selection may be ineffective for such traits (Table 4).

**Table 4. Estimation of genetic parameters**

Traits	Average	$\sigma^2_g$	$\sigma^2_p$	coefficient Variation GCV	Of PCV	H <sup>2</sup> <sub>bs</sub> (Broad Sense)	GA	GAM
LA	47.03	231.53	256.32	32.34	34.03	0.90	29.79	63.33
SPAD	36.76	24.67	26.78	13.51	14.08	0.92	9.82	26.72
PH	117.75	1165.30	1210.30	28.99	29.55	0.96	69.00	58.60
PL	24.82	7.66	10.40	11.15	12.99	0.74	4.89	19.72
TW	22.47	22.43	26.39	21.07	22.86	0.85	8.99	40.02
HI	0.35	0.01	0.01	32.29	33.80	0.91	0.22	63.55
BD	90.39	432.07	438.17	23.00	23.16	0.99	42.52	47.04
HD	97.78	471.97	474.77	22.22	22.28	0.99	44.62	45.63
FD	99.84	436.93	440.43	20.94	21.02	0.99	42.89	42.96
FGPP	187.53	8141.67	9645.67	48.11	52.37	0.84	170.77	91.06
F%	84.60	133.04	174.28	13.63	15.60	0.76	20.76	24.54
ETM	72.96	108.63	132.19	14.29	15.76	0.82	19.46	26.68
MD	142.12	305.99	312.68	12.31	12.44	0.98	35.65	25.08
GY	4.07	0.93	1.17	23.71	26.65	0.79	1.76	43.48

LA= flag leaf area 60 DAT, SPAD=chlorophyll content 60DAT, PH=plant height 90DAT, PL=panicle length, TW=thousand grain weight,HI= harvest index,BD=Days to 50% booting,HD= Days to 50% heading, FD= Days to 50% flowering, FGPP=filled grain per panicle, F%=fertility percent,ETM=effective tiller per meter square,MD=maturity days, GY=grain yield

### Principal component analysis (PCA)

Fourteen morpho-physiological parameters were recorded in eleven rice genotypes and they were grouped into PCs. The first three PCs showed eigen value more than one and they described 84% of the total variation present in genotypes. Highest amount of variation was accounted by PC1 (40%) followed by PC2 (29%) and PC3 (15%). (Table 6) Highest positive component loading for the PC1 was obtained from HI (0.365) followed by TW (0.325), F% (0.239) and so on while negative factor loading for PC1 was obtained from BD (-0.380), HD (-0.378), FD (-0.374) and MD (-0.338). Similarly, PC 2 was positively related to all the parameters except TW and HI. While PC 3 had negative loadings from all the traits except F%, PH, PL, ETM and FGPP.

According to [Chahal & Gosal \(2002\)](#), (Figure 1 and Figure 2) principal components analysis plays a major role in grouping of genotypes based on the traits. The traits having absolute value closer to 1 in PC1 affects the clustering more while the traits having value closer to 0 influence less to the clustering (Table 5).

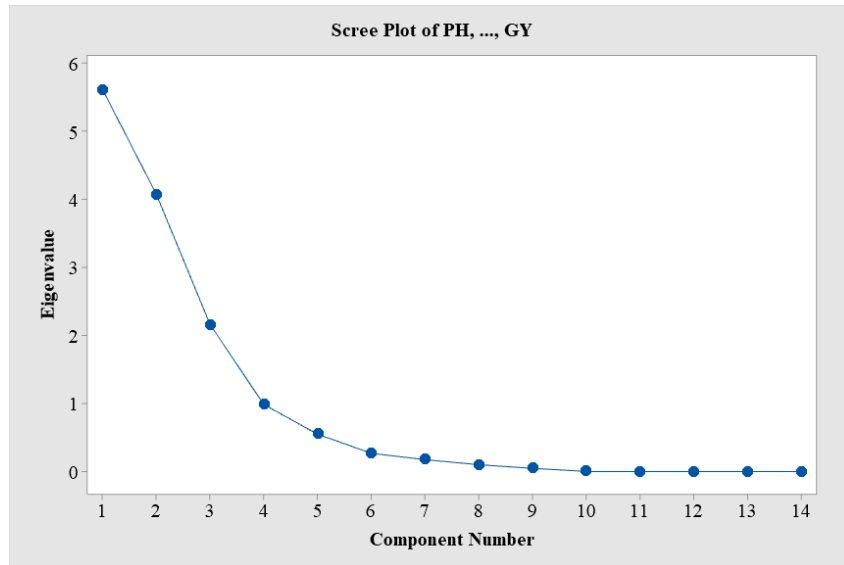
**Table 5. Variance analysis of principal components of selected traits of rice genotypes**

	PC1	PC2	PC3
Eigenvalue	5.62	4.08	2.16
Proportion	0.40	0.29	0.15
Cumulative	0.40	0.69	0.84

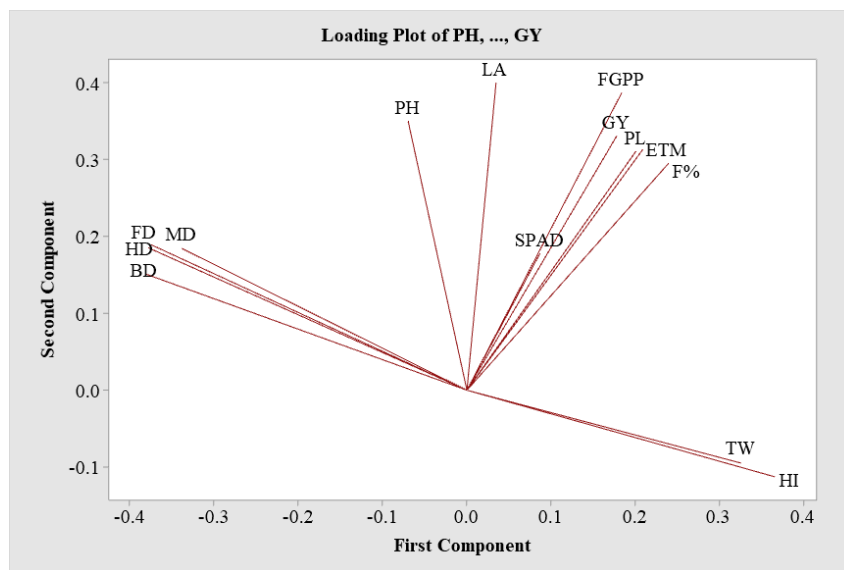
**Table 6. Eigen vector analysis of principal components of selected traits of rice genotypes**

Variable	PC1	PC2	PC3
PH	<b>-0.070</b>	0.349	0.389
LA	0.035	0.399	-0.150
PL	0.200	0.310	0.107
ETM	0.209	0.313	0.263
FGPP	0.184	0.386	0.002
SPAD	0.086	0.177	-0.510
TW	0.325	-0.095	-0.389
F%	0.239	0.294	0.243
FD	-0.374	0.189	-0.112
HD	-0.378	0.185	-0.091
BD	-0.380	0.150	-0.151
MD	-0.338	0.184	-0.207
HI	0.365	-0.112	-0.177
GY	0.178	0.330	-0.398

LA= flag leaf area 60 DAT, SPAD=chlorophyll content 60DAT, PH=plant height 90DAT, PL=panicle length, TW=thousand grain weight, HI= harvest index, BD=Days to 50% booting, HD= Days to 50% heading, FD= Days to 50% flowering, FGPP=filled grain per panicle, F%=fertility percent, ETM=effective tiller per meter square, MD=maturity days, GY=grain yield



**Figure 1. Scree plot diagram of Principal Components**



**Figure 2. Principal Component biplot of different morpho-physiological traits of rice**

### Cluster analysis

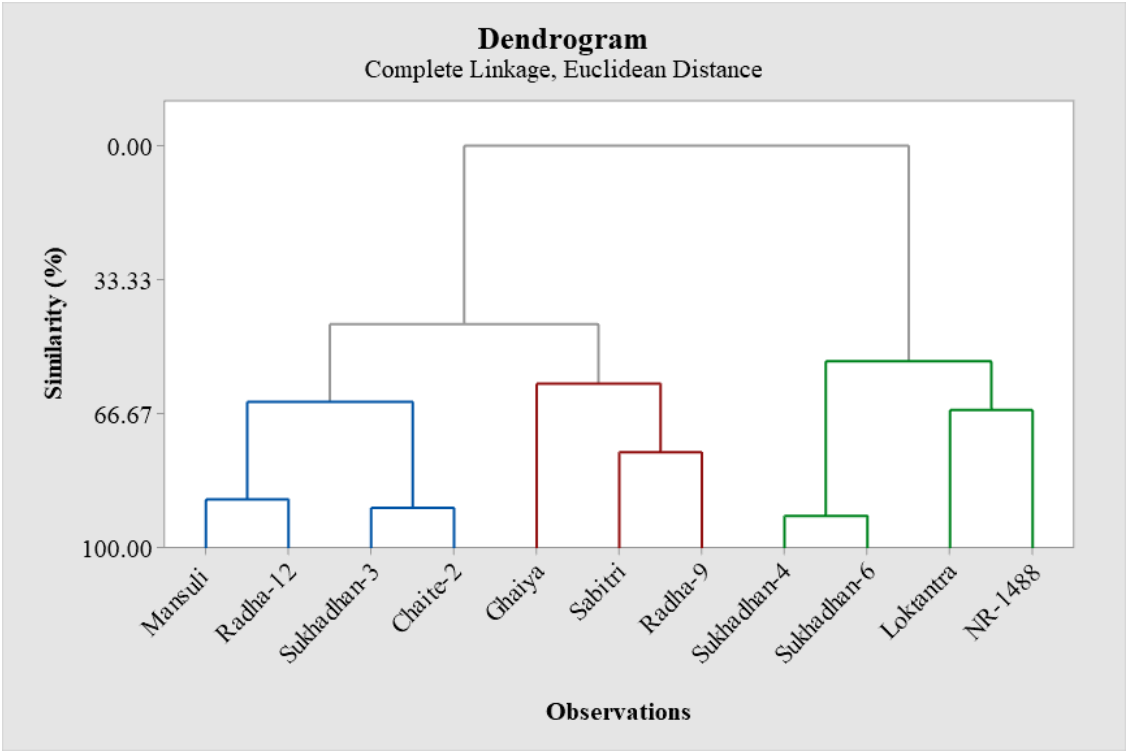
The goal of cluster analysis, a type of multivariate approach, is to mathematically group together individuals with similar descriptions into one cluster by using the traits they share to categorize them into groups of individuals or objects. The resulting cluster of individuals ought to have more homogeneity within clusters and more heterogeneity between clusters (Hair et al., 1995). Eleven genotypes of rice were grouped into three clusters by using complete linkage method and Euclidean distance.

Genotypes clustering explained 53.58% similarity which is presented in the dendrogram. Similar to this, Yousuf et al. (2008) identified four separate clusters from 70 wheat



genotypes, while [Khodadadi et al. \(2011\)](#) divided wheat cultivars into seven groups. (Figure 3) Cluster 1 consisted four genotypes which are Mansuli, Radha-12, Sukhadhan-3 and Chaite-2. Genotypes of this cluster recorded highest effective tillers per meter square (76.050) and lowest MD (140.500) and TW (22.043 gm). Genotypes of this cluster undergone phenological changes in booting, heading and flowering at 92.6, 99.9 and 101.7 days after sowing respectively.

This cluster has 114.6 cm PH, 44.195 cm<sup>2</sup> LA, 24.355 cm PL, 175.500 FGPP, 37.1 SPAD reading, 88.2% F% and 3.89 ton/ha GY (Table 7). Ghaiya, Sabitri and Radha-9 were the genotypes grouped under in cluster 2. This cluster recorded lowest values for all the traits except TW, FD, HD and BD. Genotypes of this cluster mature at last as compared to other clusters. Cluster 3 comprised of Sukhadhan-4, Sukhadhan-6, Loktantra and NR-1488. Genotypes belonging to this cluster recorded highest values for traits like PH, LA, PL, FGPP, SPAD value, TW, F%, HI and GY. This cluster had longest period for BD, HD and FD.



**Figure 3. Dendrogram showing different clusters of rice genotypes**

**Table 7. Mean value for different traits of five clusters of rice genotypes**

Variable	Cluster1	Cluster2	Cluster3	Grand centroid
PH	114.623	106.020	129.690	117.755
LA	44.195	41.317	54.165	47.035
PL	24.355	23.823	26.038	24.822
ETM	76.050	64.947	75.877	72.959
FGPP	175.500	123.840	247.335	187.533
SPAD	37.125	35.467	37.345	36.753
TW	22.043	22.487	22.883	22.469
F%	88.235	74.820	88.300	84.600
FD	101.750	100.670	97.338	99.851
HD	99.918	98.670	95.002	97.790
BD	92.665	91.667	87.165	90.393
MD	140.500	146.443	140.502	142.122
HI	0.343	0.337	0.355	0.345
GY	3.893	3.670	4.527	4.063

LA= flag leaf area 60 DAT, SPAD=chlorophyll content 60DAT, PH=plant height 90DAT, PL=panicle length, TW=thousand grain weight, HI= harvest index, BD=Days to 50% booting, HD= Days to 50% heading, FD= Days to 50% flowering, FGPP=filled grain per panicle, F%=fertility percent, ETM=effective tiller per meter square, MD=maturity days, GY=grain yield

**Table 8. Euclidean distance matrix analysis of three clusters of rice genotypes**

	Cluster1	Cluster2
Cluster1		
Cluster2	55.6472	
Cluster3	74.5962	127.934

Maximum distance was observed between cluster 2 and cluster 3 (127.934) followed by distance between cluster 1 and cluster 3 (74.5962) (Table 8). This shows the diversified nature of genotypes present in these clusters and they can be used for transgressive breeding. Lowest distance was seen between cluster 1 and 2 (55.6472).

## CONCLUSION

Significant differences for all traits studied were observed as revealed by analysis of variance (ANOVA), which suggests prevalence of ample genetic variability. Yield trait is considered as most important criteria for evaluating drought tolerance among varieties. From the research, it was recorded that variety Sukhadhan-4, Sukhadhan-6 and NR-1488 had higher mean yield. So, it can be concluded that they are suitable to be adopted for cultivation in Lamjung in rainy condition while lowest mean value for yield was found for Ghaiya which is not suitable to be recommended for cultivation in Lamjung area. High GCV and PCV was observed for FGPP followed by LA, HI, PH, BD, MD, TW and FD. Similarly relatively moderate values of GCV and PCV was observed for ETM followed by F%, SPAD, MD and PL. High GCV signifies present of high variation among genotypes with respect to these characters and also PCV was higher than GCV for all traits under study and difference between them was found low, meaning less influence of environment in the expression of these characters and selection could be effective on the basis of phenotype for the

improvement of these traits. High heritability was recorded for all the traits studied. Highest heritability was found for HD, booting and flowering followed by MD, PH, SPAD, HI, LA, TW, FGPP, ETM, GY, F% and PL. Similarly, high genetic advance as percentage of mean was observed for all the traits studied except PL. Highest value of GAM was observed for FGPP followed by HI, LA, PH, BD, HD, GY, FD, TW, SPAD, ETM, MD, F% and PL. Moderate GAM was recorded for PL. Heritability estimates alone is not sufficient rather than high heritability along with high GAM would be effective for selecting superior varieties which is the contribution of additive gene action.

High heritability along with high genetic advance expressed as percentage of mean was found for traits such as HI, LA, PH, FGPP, BD and HD, which indicates that heritability is due to the additive gene action and selection may be effective for such traits. While low heritability along with low GAM was found in traits like F% and PL indicating non-additive gene action and selection may be ineffective for such traits. Correlation studies showed that SPAD, LA and FGPP had positive and significant association with GY which indicates that indirect selection of these characters would directly affects the expression of GY. Among 14 PCs, 3 PCs were extracted accounting 84% of the total variation. Highest positive component loading for the PC1 was obtained from HI followed by TW, F% and so on while negative factor loading for PC1 was obtained from BD, HD, FD and MD. Hence, PCA helps to know the variation present in the genotypes which aids in the direct selection of superior rice genotypes.

Three clusters of rice were observed from cluster analysis. Genotypes of rice having enough divergence i.e. Euclidean distance can be used for transgressive breeding giving choices for diverse parents selection. Cluster 3 was superior for yield and yield attributing characters and hence genotypes belonging to this cluster can be used for rice improvement program. Sukhadhan-4 recorded highest GY (5 tons/ha) with higher values of FGPP, TW, PL, ETM, F%, leaf area and SPAD.

#### **AUTHOR CONTRIBUTIONS**

All authors have contributed equally during initial manuscript preparation and the work of further reviewing and editing of manuscript till publication was done by Bigyan K.C.

#### **COMPETING INTERESTS**

The authors declare they have no conflict of interest. The manuscript has not been submitted for publication in other journal.

#### **ETHICS APPROVAL**

Not applicable

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